

XSPAN - A Cross-Species Anatomy Network**Webber, Bonnie****University of Edinburgh, Edinburgh, UK**

XSPAN aims to support cross-species access to tissue-based genetic information through an internet-based cross-species anatomy ontology integration system. This system will provide interoperability between anatomy databases of key model embryos (drosophila, mouse, zebrafish, c.elegans and hum), which should, in turn, facilitate access to gene expression and other tissue-based data across species. Currently, two sources of mappings between tissues are being explored: (a) domain experts and (b) tissue-related data sets.

With respect to (a), we are developing tools and resources to enable domain expert to manually record their knowledge of cross-species tissue mappings, including *tissue homology*, *cell function homology*, *analogy* and *association*, and to make that knowledge accessible through the Internet. The system as a whole will be based on a set of anatomy and cell-type ontologies, together with a database of mapping information that incorporates the cross-anatomy mappings.

One obstacle to acquiring cross-species tissue mappings has been differences in the anatomy ontologies of different species. Of necessity, anatomy ontologies differ due to the different developmental patterns and structures of the organisms concerned. However, these differences have been unnecessarily compounded by differences in terminology and in the ways that ontological relations have been used and interpreted. For example, the mouse anatomy (<http://genex.hgu.mrc.ac.uk/Databases/Anatomy/>) uses only a *part-of* relation, while the drosophila anatomy (<http://flybase.bio.indiana.edu>) uses *isa*, *part-of* and *lineage*. (Work is in progress on adding lineage to the mouse anatomy, but differences between anatomies remain.

As long as anatomies are primarily used by humans, such differences have few serious consequences. But they limit any attempt to establish links between anatomies that can be checked for consistency [Aitken, 2004]. To overcome this obstacle, we have proposed an RDF schema that clarifies the meaning of GO relationships and provides an extensible framework for both syntax and semantics.

With respect to (b), we are exploring cross-species tissue mappings based on expression patterns in genes that are homologous across pairs of species. A data warehouse is being developed that will support data mining of gene-expression patterns across model organisms. Where significant levels of co-expression can be found for gene homologues, users can be alerted to this as a basis for asserting a cross-species mapping at the tissue level. To facilitate such data mining, a distributed system is being developed which provides access to the underlying anatomy ontology and gene-expression data through standardized Web Services, and which interoperates with a BLAST service.

Access to XSPAN will be provided at the user level, through an appropriate set of graphical user interfaces, as well as at the programmatic level, through a number of Web and/or Grid Services. The latter is intended to enable XSPAN to become part of a wider Bioinformatics Grid.

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Reference

[Aitken, 2004] J.S. Aitken, B.L. Webber, J.B.L. Bard. Anatomy Ontologies and Cross-Species Tissue Homologies. Submitted to the *Pacific Symposium on Biocomputing*, 2004.